

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: OSUMI Chieko  
NOZAKI Jinshi  
KIDA Takao
- (ii) TITLE OF INVENTION: RAFFINOSE SYNTHASE GENE, METHOD FOR  
PRODUCING RAFFINOSE, AND TRANSGENIC PLANT
- (iii) NUMBER OF SEQUENCES: 22
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
  - (B) STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
  - (C) CITY: ARLINGTON
  - (D) STATE: VIRGINIA
  - (E) COUNTRY: USA
  - (F) ZIP: 22202
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
- (vi) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: NORMAN F. OBLON
  - (B) REGISTRATION NUMBER: 24,618
- (vii) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (703)-413-3000
  - (B) TELEFAX: (703)-413-2220

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu	Thr	Val	His	Pro	Gln
1				5					10					15	
Gly	Val	Ile	Glu	Gly	Val	Arg	His	Leu	Val	Asp	Gly	Gly	Cys		
			20					25					30		

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro Val Ser Val Gly Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp  
1 5 10 15  
Ser Arg His

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Tyr Asp Gln Asp Gln Met Val Val Val Gln Val Pro Trp Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2517 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: cucumber (Cucumis sativas)

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 56..2407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AAAAACAAC CCTTCTTTTA GTTTTTTGGG TTTGTTTCTT CTTTTCTTCT CACAA ATG 58  
Met  
1  
GCT CCT AGT TTT AAA AAT GGT GGC TCC AAC GTA GTT TCA TTT GAT GGC 106  
Ala Pro Ser Phe Lys Asn Gly Gly Ser Asn Val Val Ser Phe Asp Gly  
5 10 15  
TTA AAT GAC ATG TCG TCA CCG TTT GCA ATC GAC GGA TCG GAT TTC ACT 154  
Leu Asn Asp Met Ser Ser Pro Phe Ala Ile Asp Gly Ser Asp Phe Thr  
20 25 30  
GTG AAC GGT CAT TCG TTT CTG TCC GAT GTT CCT GAG AAC ATT GTT GCT 202  
Val Asn Gly His Ser Phe Leu Ser Asp Val Pro Glu Asn Ile Val Ala  
35 40 45  
TCT CCT TCT CCG TAC ACT TCG ATA GAC AAG TCC CCG GTT TCG GTT GGT 250  
Ser Pro Ser Pro Tyr Thr Ser Ile Asp Lys Ser Pro Val Ser Val Gly  
50 55 60 65  
TGC TTT GTT GGA TTC GAC GCG TCG GAA CCT GAT AGC CGA CAT GTT GTT 298  
Cys Phe Val Gly Phe Asp Ala Ser Glu Pro Asp Ser Arg His Val Val  
70 75 80  
TCG ATT GGG AAG CTG AAG GAT ATT CGG TTT ATG AGT ATT TTC AGG TTT 346  
Ser Ile Gly Lys Leu Lys Asp Ile Arg Phe Met Ser Ile Phe Arg Phe

				85				90				95					
AAG	GTT	TGG	TGG	ACT	ACA	CAC	TGG	GTT	GGT	CGA	AAT	GGT	GGG	GAT	CTT	394	
Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Arg	Asn	Gly	Gly	Asp	Leu		
100								105				110					
GAA	TCG	GAG	ACT	CAG	ATT	GTG	ATC	CTT	GAG	AAG	TCA	GAT	TCT	GGT	CGA	442	
Glu	Ser	Glu	Thr	Gln	Ile	Val	Ile	Leu	Glu	Lys	Ser	Asp	Ser	Gly	Arg		
115								120				125					
CCG	TAT	GTT	TTC	CTT	CTT	CCG	ATC	GTT	GAG	GGA	CCG	TTC	CGA	ACC	TCG	490	
Pro	Tyr	Val	Phe	Leu	Leu	Pro	Ile	Val	Glu	Gly	Pro	Phe	Arg	Thr	Ser		
130				135								140				145	
ATT	CAG	CCT	GGG	GAT	GAT	GAC	TTT	GTC	GAT	GTT	TGT	GTC	GAG	AGT	GGT	538	
Ile	Gln	Pro	Gly	Asp	Asp	Asp	Phe	Val	Asp	Val	Cys	Val	Glu	Ser	Gly		
150								155				160					
TCG	TCG	AAA	GTT	GTT	GAT	GCA	TCG	TTC	CGA	AGT	ATG	TTG	TAT	CTT	CAT	586	
Ser	Ser	Lys	Val	Val	Asp	Ala	Ser	Phe	Arg	Ser	Met	Leu	Tyr	Leu	His		
165								170				175					
GCT	GGT	GAT	GAT	CCG	TTT	GCA	CTT	GTT	AAA	GAG	GCG	ATG	AAG	ATC	GTG	634	
Ala	Gly	Asp	Asp	Pro	Phe	Ala	Leu	Val	Lys	Glu	Ala	Met	Lys	Ile	Val		
180								185				190					
AGG	ACC	CAT	CTT	GGA	ACT	TTT	CGC	TTG	TTG	GAG	GAG	AAG	ACT	CCA	CCA	682	
Arg	Thr	His	Leu	Gly	Thr	Phe	Arg	Leu	Leu	Glu	Glu	Lys	Thr	Pro	Pro		
195								200				205					
GGT	ATC	GTG	GAC	AAA	TTC	GGT	TGG	TGC	ACG	TGG	GAC	GCG	TTT	TAC	CTA	730	
Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr	Leu		
210				215								220				225	
ACG	GTT	CAT	CCA	CAG	GGC	GTA	ATA	GAA	GGC	GTG	AGG	CAT	CTC	GTC	GAC	778	
Thr	Val	His	Pro	Gln	Gly	Val	Ile	Glu	Gly	Val	Arg	His	Leu	Val	Asp		
230								235				240					
GGC	GGT	TGT	CCT	CCC	GGT	TTA	GTC	CTA	ATC	GAC	GAT	GGT	TGG	CAA	TCC	826	
Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp	Asp	Gly	Trp	Gln	Ser		
245								250				255					
ATC	GGA	CAC	GAT	TCG	GAT	CCC	ATC	ACC	AAA	GAA	GGA	ATG	AAC	CAA	ACC	874	
Ile	Gly	His	Asp	Ser	Asp	Pro	Ile	Thr	Lys	Glu	Gly	Met	Asn	Gln	Thr		
260								265				270					
GTC	GCC	GGC	GAG	CAA	ATG	CCC	TGC	CGT	CTT	TTG	AAA	TTC	CAA	GAG	AAT	922	
Val	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Leu	Lys	Phe	Gln	Glu	Asn		
275								280				285					
TAC	AAA	TTC	CGT	GAC	TAC	GTC	AAT	CCC	AAG	GCC	ACC	GGC	CCC	CGA	GCC	970	
Tyr	Lys	Phe	Arg	Asp	Tyr	Val	Asn	Pro	Lys	Ala	Thr	Gly	Pro	Arg	Ala		
290				295								300				305	
GGC	CAG	AAG	GGG	ATG	AAG	GCG	TTT	ATA	GAT	GAA	CTC	AAA	GGA	GAG	TTT	1018	
Gly	Gln	Lys	Gly	Met	Lys	Ala	Phe	Ile	Asp	Glu	Leu	Lys	Gly	Glu	Phe		
310								315				320					
AAG	ACT	GTG	GAG	CAT	GTT	TAT	GTT	TGG	CAT	GCT	TTG	TGT	GGA	TAT	TGG	1066	
Lys	Thr	Val	Glu	His	Val	Tyr	Val	Trp	His	Ala	Leu	Cys	Gly	Tyr	Trp		
325								330				335					
GGT	GGC	CTT	CGC	CCG	CAG	GTG	CCT	GGC	TTG	CCT	GAG	GCA	CGT	GTG	ATT	1114	
Gly	Gly	Leu	Arg	Pro	Gln	Val	Pro	Gly	Leu	Pro	Glu	Ala	Arg	Val	Ile		
340								345				350					

CAG	CCA	GTG	CTT	TCA	CCA	GGG	CTG	CAG	ATG	ACG	ATG	GAG	GAT	TTG	GCG	1162
Gln	Pro	Val	Leu	Ser	Pro	Gly	Leu	Gln	Met	Thr	Met	Glu	Asp	Leu	Ala	
355						360					365					
GTG	GAT	AAG	ATT	GTT	CTT	CAT	AAG	GTC	GGG	CTG	GTC	CCG	CCG	GAG	AAG	1210
Val	Asp	Lys	Ile	Val	Leu	His	Lys	Val	Gly	Leu	Val	Pro	Pro	Glu	Lys	
370					375				380						385	
GCT	GAG	GAG	ATG	TAC	GAA	GGA	CTT	CAT	GCT	CAT	TTG	GAA	AAA	GTT	GGG	1258
Ala	Glu	Glu	Met	Tyr	Glu	Gly	Leu	His	Ala	His	Leu	Glu	Lys	Val	Gly	
				390					395					400		
ATC	GAC	GGT	GTT	AAG	ATT	GAC	GTT	ATC	CAC	CTA	TTG	GAG	ATG	TTG	TGT	1306
Ile	Asp	Gly	Val	Lys	Ile	Asp	Val	Ile	His	Leu	Leu	Glu	Met	Leu	Cys	
			405					410					415			
GAA	GAC	TAT	GGA	GGG	AGA	GTG	GAT	TTG	GCA	AAG	GCA	TAT	TAC	AAA	GCA	1354
Glu	Asp	Tyr	Gly	Gly	Arg	Val	Asp	Leu	Ala	Lys	Ala	Tyr	Tyr	Lys	Ala	
		420					425					430				
ATG	ACC	AAA	TCA	ATA	AAT	AAA	CAT	TTT	AAA	GGA	AAT	GGA	GTC	ATT	GCA	1402
Met	Thr	Lys	Ser	Ile	Asn	Lys	His	Phe	Lys	Gly	Asn	Gly	Val	Ile	Ala	
		435				440						445				
AGT	ATG	GAA	CAT	TGT	AAC	GAC	TTC	ATG	TTC	CTT	GGC	ACG	GAA	GCT	ATC	1450
Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	Gly	Thr	Glu	Ala	Ile	
450					455					460					465	
TCT	GTT	GGT	CGT	GTT	GGT	GAT	GAC	TTT	TGG	TGC	ACG	GAC	CCC	TCT	GGT	1498
Ser	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	Asp	Pro	Ser	Gly	
				470					475					480		
GAT	CCA	AAC	GGT	ACG	TTT	TGG	CTC	CAA	GGA	TGT	CAC	ATG	GTT	CAT	TGT	1546
Asp	Pro	Asn	Gly	Thr	Phe	Trp	Leu	Gln	Gly	Cys	His	Met	Val	His	Cys	
			485				490					495				
GCC	AAC	GAC	AGC	TTG	TGG	ATG	GGG	AAC	TTC	ATC	CAC	CCT	GAC	TGG	GAT	1594
Ala	Asn	Asp	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	His	Pro	Asp	Trp	Asp	
		500					505					510				
ATG	TTC	CAA	TCC	ACC	CAC	CCT	TGT	GCC	GCC	TTC	CAT	GCT	GCC	TCT	CGA	1642
Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Ala	Phe	His	Ala	Ala	Ser	Arg	
		515				520						525				
GCC	ATC	TCT	GGT	GGC	CCG	ATC	TAT	GTT	AGT	GAT	TCT	GTG	GGA	AAG	CAT	1690
Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	Ser	Val	Gly	Lys	His	
530					535					540					545	
AAC	TTT	GAT	CTT	CTG	AAA	AAA	CTA	GTG	CTT	CCT	GAT	GGA	TCG	ATC	CTT	1738
Asn	Phe	Asp	Leu	Leu	Lys	Lys	Leu	Val	Leu	Pro	Asp	Gly	Ser	Ile	Leu	
				550					555					560		
CGA	AGT	GAG	TAC	TAT	GCA	CTC	CCG	ACT	CGC	GAT	TGT	TTG	TTT	GAA	GAC	1786
Arg	Ser	Glu	Tyr	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Cys	Leu	Phe	Glu	Asp	
			565					570					575			
CCT	TTG	CAT	AAT	GGA	GAA	ACT	ATG	CTT	AAG	ATT	TGG	AAT	CTC	AAC	AAG	1834
Pro	Leu	His	Asn	Gly	Glu	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn	Lys	
		580					585					590				
TTC	ACT	GGA	GTG	ATT	GGT	GCA	TTC	AAC	TGC	CAA	GGA	GGA	GGA	TGG	TGT	1882
Phe	Thr	Gly	Val	Ile	Gly	Ala	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp	Cys	
		595				600					605					
CGT	GAG	ACA	CGC	CGC	AAC	CAA	TGC	TTT	TCA	CAA	TAC	TCA	AAA	CGA	GTG	1930

Arg	Glu	Thr	Arg	Arg	Asn	Gln	Cys	Phe	Ser	Gln	Tyr	Ser	Lys	Arg	Val		
610					615					620					625		
ACA	TCC	AAA	ACT	AAC	CCA	AAA	GAC	ATA	GAA	TGG	CAC	AGT	GGA	GAA	AAC	1978	
Thr	Ser	Lys	Thr	Asn	Pro	Lys	Asp	Ile	Glu	Trp	His	Ser	Gly	Glu	Asn		
				630					635					640			
CCT	ATC	TCT	ATT	GAA	GGC	GTT	AAA	ACC	TTT	GCG	CTT	TAC	CTC	TAT	CAA	2026	
Pro	Ile	Ser	Ile	Glu	Gly	Val	Lys	Thr	Phe	Ala	Leu	Tyr	Leu	Tyr	Gln		
			645					650					655				
GCC	AAA	AAA	CTT	ATC	CTC	TCC	AAG	CCC	TCT	CAA	GAT	CTT	GAC	ATA	GCT	2074	
Ala	Lys	Lys	Leu	Ile	Leu	Ser	Lys	Pro	Ser	Gln	Asp	Leu	Asp	Ile	Ala		
		660					665				670						
CTT	GAC	CCA	TTC	GAA	TTC	GAG	CTC	ATC	ACT	GTT	TCA	CCA	GTG	ACC	AAA	2122	
Leu	Asp	Pro	Phe	Glu	Phe	Glu	Leu	Ile	Thr	Val	Ser	Pro	Val	Thr	Lys		
	675					680				685							
CTC	ATC	CAA	ACT	TCT	CTA	CAC	TTT	GCC	CCA	ATT	GGG	CTG	GTG	AAC	ATG	2170	
Leu	Ile	Gln	Thr	Ser	Leu	His	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	Met		
690					695				700					705			
CTT	AAC	ACT	AGT	GGA	GCC	ATC	CAA	TCT	GTG	GAC	TAT	GAC	GAT	GAC	CTA	2218	
Leu	Asn	Thr	Ser	Gly	Ala	Ile	Gln	Ser	Val	Asp	Tyr	Asp	Asp	Asp	Leu		
				710				715					720				
AGC	TCA	GTC	GAG	ATT	GGT	GTC	AAA	GGG	TGT	GGT	GAG	ATG	CGA	GTA	TTT	2266	
Ser	Ser	Val	Glu	Ile	Gly	Val	Lys	Gly	Cys	Gly	Glu	Met	Arg	Val	Phe		
		725					730					735					
GCA	TCG	AAA	AAA	CCA	AGG	GCT	TGT	CGT	ATT	GAT	GGG	GAG	GAT	GTT	GGG	2314	
Ala	Ser	Lys	Lys	Pro	Arg	Ala	Cys	Arg	Ile	Asp	Gly	Glu	Asp	Val	Gly		
		740				745					750						
TTC	AAG	TAT	GAT	CAG	GAC	CAA	ATG	GTG	GTG	GTT	CAA	GTG	CCA	TGG	CCA	2362	
Phe	Lys	Tyr	Asp	Gln	Asp	Gln	Met	Val	Val	Val	Gln	Val	Pro	Trp	Pro		
	755				760				765								
ATT	GAT	TCT	TCA	TCG	GGT	GGC	ATT	TCG	GTT	ATC	GAG	TAC	TTG	TTT		2407	
Ile	Asp	Ser	Ser	Ser	Gly	Gly	Ile	Ser	Val	Ile	Glu	Tyr	Leu	Phe			
770					775				780								
TAATTTT	TAT	TTATG	TAAAGC	TCAATG	GATTG	TTGTTG	TGTG	CGCTG	TGTG	TGTT	GCTAT	CAATG				2467	
TATTTCT	CTC	CAAAG	AAAAA	TTATGT	GTAA	TTTG	GAGAGT	AATTA	AGTGA							2517	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 784 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	Pro	Ser	Phe	Lys	Asn	Gly	Gly	Ser	Asn	Val	Val	Ser	Phe	Asp
1				5				10					15		
Gly	Leu	Asn	Asp	Met	Ser	Ser	Pro	Phe	Ala	Ile	Asp	Gly	Ser	Asp	Phe
		20					25				30				
Thr	Val	Asn	Gly	His	Ser	Phe	Leu	Ser	Asp	Val	Pro	Glu	Asn	Ile	Val
	35					40				45					
Ala	Ser	Pro	Ser	Pro	Tyr	Thr	Ser	Ile	Asp	Lys	Ser	Pro	Val	Ser	Val

50		55		60											
Gly	Cys	Phe	Val	Gly	Phe	Asp	Ala	Ser	Glu	Pro	Asp	Ser	Arg	His	Val
65					70					75					80
Val	Ser	Ile	Gly	Lys	Leu	Lys	Asp	Ile	Arg	Phe	Met	Ser	Ile	Phe	Arg
				85					90					95	
Phe	Lys	Val	Trp	Trp	Thr	Thr	His	Trp	Val	Gly	Arg	Asn	Gly	Gly	Asp
			100					105					110		
Leu	Glu	Ser	Glu	Thr	Gln	Ile	Val	Ile	Leu	Glu	Lys	Ser	Asp	Ser	Gly
		115					120					125			
Arg	Pro	Tyr	Val	Phe	Leu	Leu	Pro	Ile	Val	Glu	Gly	Pro	Phe	Arg	Thr
	130					135					140				
Ser	Ile	Gln	Pro	Gly	Asp	Asp	Asp	Phe	Val	Asp	Val	Cys	Val	Glu	Ser
145					150					155					160
Gly	Ser	Ser	Lys	Val	Val	Asp	Ala	Ser	Phe	Arg	Ser	Met	Leu	Tyr	Leu
			165						170					175	
His	Ala	Gly	Asp	Asp	Pro	Phe	Ala	Leu	Val	Lys	Glu	Ala	Met	Lys	Ile
		180						185					190		
Val	Arg	Thr	His	Leu	Gly	Thr	Phe	Arg	Leu	Leu	Glu	Glu	Lys	Thr	Pro
	195						200					205			
Pro	Gly	Ile	Val	Asp	Lys	Phe	Gly	Trp	Cys	Thr	Trp	Asp	Ala	Phe	Tyr
210						215					220				
Leu	Thr	Val	His	Pro	Gln	Gly	Val	Ile	Glu	Gly	Val	Arg	His	Leu	Val
225					230					235					240
Asp	Gly	Gly	Cys	Pro	Pro	Gly	Leu	Val	Leu	Ile	Asp	Asp	Gly	Trp	Gln
			245					250						255	
Ser	Ile	Gly	His	Asp	Ser	Asp	Pro	Ile	Thr	Lys	Glu	Gly	Met	Asn	Gln
	260						265						270		
Thr	Val	Ala	Gly	Glu	Gln	Met	Pro	Cys	Arg	Leu	Leu	Lys	Phe	Gln	Glu
	275					280						285			
Asn	Tyr	Lys	Phe	Arg	Asp	Tyr	Val	Asn	Pro	Lys	Ala	Thr	Gly	Pro	Arg
290					295						300				
Ala	Gly	Gln	Lys	Gly	Met	Lys	Ala	Phe	Ile	Asp	Glu	Leu	Lys	Gly	Glu
305					310					315					320
Phe	Lys	Thr	Val	Glu	His	Val	Tyr	Val	Trp	His	Ala	Leu	Cys	Gly	Tyr
			325						330					335	
Trp	Gly	Gly	Leu	Arg	Pro	Gln	Val	Pro	Gly	Leu	Pro	Glu	Ala	Arg	Val
			340					345					350		
Ile	Gln	Pro	Val	Leu	Ser	Pro	Gly	Leu	Gln	Met	Thr	Met	Glu	Asp	Leu
	355						360					365			
Ala	Val	Asp	Lys	Ile	Val	Leu	His	Lys	Val	Gly	Leu	Val	Pro	Pro	Glu
	370					375					380				
Lys	Ala	Glu	Glu	Met	Tyr	Glu	Gly	Leu	His	Ala	His	Leu	Glu	Lys	Val
385					390					395					400
Gly	Ile	Asp	Gly	Val	Lys	Ile	Asp	Val	Ile	His	Leu	Leu	Glu	Met	Leu
			405						410					415	
Cys	Glu	Asp	Tyr	Gly	Gly	Arg	Val	Asp	Leu	Ala	Lys	Ala	Tyr	Tyr	Lys
	420							425					430		
Ala	Met	Thr	Lys	Ser	Ile	Asn	Lys	His	Phe	Lys	Gly	Asn	Gly	Val	Ile
	435						440						445		

Ala	Ser	Met	Glu	His	Cys	Asn	Asp	Phe	Met	Phe	Leu	Gly	Thr	Glu	Ala	450	455	460
Ile	Ser	Leu	Gly	Arg	Val	Gly	Asp	Asp	Phe	Trp	Cys	Thr	Asp	Pro	Ser	465	470	475
Gly	Asp	Pro	Asn	Gly	Thr	Phe	Trp	Leu	Gln	Gly	Cys	His	Met	Val	His	485	490	495
Cys	Ala	Asn	Asp	Ser	Leu	Trp	Met	Gly	Asn	Phe	Ile	His	Pro	Asp	Trp	500	505	510
Asp	Met	Phe	Gln	Ser	Thr	His	Pro	Cys	Ala	Ala	Phe	His	Ala	Ala	Ser	515	520	525
Arg	Ala	Ile	Ser	Gly	Gly	Pro	Ile	Tyr	Val	Ser	Asp	Ser	Val	Gly	Lys	530	535	540
His	Asn	Phe	Asp	Leu	Leu	Lys	Lys	Leu	Val	Leu	Pro	Asp	Gly	Ser	Ile	545	550	555
Leu	Arg	Ser	Glu	Tyr	Tyr	Ala	Leu	Pro	Thr	Arg	Asp	Cys	Leu	Phe	Glu	565	570	575
Asp	Pro	Leu	His	Asn	Gly	Glu	Thr	Met	Leu	Lys	Ile	Trp	Asn	Leu	Asn	580	585	590
Lys	Phe	Thr	Gly	Val	Ile	Gly	Ala	Phe	Asn	Cys	Gln	Gly	Gly	Gly	Trp	595	600	605
Cys	Arg	Glu	Thr	Arg	Arg	Asn	Gln	Cys	Phe	Ser	Gln	Tyr	Ser	Lys	Arg	610	615	620
Val	Thr	Ser	Lys	Thr	Asn	Pro	Lys	Asp	Ile	Glu	Trp	His	Ser	Gly	Glu	625	630	635
Asn	Pro	Ile	Ser	Ile	Glu	Gly	Val	Lys	Thr	Phe	Ala	Leu	Tyr	Leu	Tyr	645	650	655
Gln	Ala	Lys	Lys	Leu	Ile	Leu	Ser	Lys	Pro	Ser	Gln	Asp	Leu	Asp	Ile	660	665	670
Ala	Leu	Asp	Pro	Phe	Glu	Phe	Glu	Leu	Ile	Thr	Val	Ser	Pro	Val	Thr	675	680	685
Lys	Leu	Ile	Gln	Thr	Ser	Leu	His	Phe	Ala	Pro	Ile	Gly	Leu	Val	Asn	690	695	700
Met	Leu	Asn	Thr	Ser	Gly	Ala	Ile	Gln	Ser	Val	Asp	Tyr	Asp	Asp	Asp	705	710	715
Leu	Ser	Ser	Val	Glu	Ile	Gly	Val	Lys	Gly	Cys	Gly	Glu	Met	Arg	Val	725	730	735
Phe	Ala	Ser	Lys	Lys	Pro	Arg	Ala	Cys	Arg	Ile	Asp	Gly	Glu	Asp	Val	740	745	750
Gly	Phe	Lys	Tyr	Asp	Gln	Asp	Gln	Met	Val	Val	Val	Gln	Val	Pro	Trp	755	760	765
Pro	Ile	Asp	Ser	Ser	Ser	Gly	Gly	Ile	Ser	Val	Ile	Glu	Tyr	Leu	Phe	770	775	780

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc= "Synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTYTAYCTBA CHGTNCAAYCC TCA

23

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTYTAYCTBA CHGTNCAAYCC CCA

23

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTYTAYCTBA CHGTNCAAYCC ACA

23

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTYTAYCTBA CHGTNCAAYCC GCA

23

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:



(D) OTHER INFORMATION: N at 6 and 11 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GARGGNGTNM GNCACTRGT NGAYGG

26

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GARGGNGTNM GNCACTYGT NGAYGG

26

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 6 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GARGGNGTNM GNCACTTRGT NGAYGG

26

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

(A) NAME/KEY:

(B) LOCATION:

(D) OTHER INFORMATION: N at 3 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTNNGNTGYT TYGTNGGYTT YGAYGC

26

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 3 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTNNGNTGYT TYGTNGGRTT YGAYGC

26

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 9 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TTYGAYGCNT CNGARCCHGA YTCDCGNCA

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 9 and 11 = inosine

Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
TTYGAYGCNT CNGARCCHGA YTCDAGYCA

30

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
GAYCARGAYC TRATGGTNGT

20

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 6 and 15 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:  
CCRTCNACYA GRTGNCKNAC NCCYTC

26

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc= "Synthetic DNA"

(ix) FEATURE:

- (A) NAME/KEY:
- (B) LOCATION:
- (D) OTHER INFORMATION: N at 6 and 15 = inosine  
Other N = A, G, C, or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:  
CCRTCNACRA GRTGNCKNAC NCCYTC

26

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc= "Synthetic DNA"  
 (ix) FEATURE:  
 (A) NAME/KEY:  
 (B) LOCATION:  
 (D) OTHER INFORMATION: N at 6 and 15 = inosine  
 Other N = A, G, C, or T  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:  
 CCRTCACYA TRTGNCKNAC NCCYTC

26

(2) INFORMATION FOR SEQ ID NO:21:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc= "Synthetic DNA"  
 (ix) FEATURE:  
 (A) NAME/KEY:  
 (B) LOCATION:  
 (D) OTHER INFORMATION: N at 3 and 18 = inosine  
 Other N = A, G, C, or T  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:  
 TGNGGHHGART CDGGYTCNGA NGCRTCRAA

29

(2) INFORMATION FOR SEQ ID NO:22:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: other nucleic acid  
 (A) DESCRIPTION: /desc= "Synthetic DNA"  
 (ix) FEATURE:  
 (A) NAME/KEY:  
 (B) LOCATION:  
 (D) OTHER INFORMATION: N at 19 = inosine  
 Other N = A, G, C, or T  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:  
 RTGRCTHGAR TCDGGYTCNG ANGRTCRAA

30